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Research article

GGE biplot and AMMI analysis for stability and adaptability of dual-purpose maize hybrids tested across multi-environments for baby corn and fodder yield

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Abstract

Meeting the growing demand for baby corn necessitates the development of dual-purpose hybrids that are both high-yielding and genetically stable. Accordingly, the present study aimed for multi-location testing of twelve newly crossed elite baby corn hybrids along with one check CMVL BABY CORN-2 across four environments during Rabi 2021-22. Analysis of variance underscored the significant impact of genetic (G), environmental (E), and their interaction (GE) on all traits under study. The environment was the most important source of variation for all the traits, followed by G (3.37–10.51%) and GE (1.03–2.77). The first two principal components explained 88.48, 87.52 and 76.03% of the total variation for DS, BCY and GFY, respectively. Environmental evaluation classified locations into three distinct mega-environments *viz*. ME I encompassed Hyderabad and Hazaribagh, and ME II and III were represented solely by Ludhiana and Varanasi, respectively. Based on the GGE biplot and AMMI analysis, genotypes T9 and T11 exhibited superior performance and stability across multiple locations over the check for both BCY and GFY traits.

Keywords: Baby corn, Fodder yield, Maize, Stability

Introduction

Baby corn, known for its tender texture and delicate flavor, is harvested immediately after silking. Due to its favorable nutrient profile and versatile culinary applications, it has gained significant recognition as a popular vegetable (Hossain *et al*., 2022). Compared to conventional corn cultivation, baby corn farming generates higher profits per unit area as it requires less land and has shorter growing periods. The cultivation of baby corn in India has experienced significant growth in recent years.

Baby corn not only functions as a valuable vegetable crop but also displays remarkable potential as a fodder resource. All parts of the plant, including the leaves, stalks, and cobs, can be used as highly nutritious green fodder. India is home to the largest and most diverse livestock population globally, with approximately 70% of households depending on the livestock and agriculture sectors for their livelihoods (Ghosh *et al*., 2016). Given the shortage of 35.6% in green fodder within the country (Anonymous, 2015), the cultivation of baby corn provides a promising solution to this issue. With its fast-growing nature and high biomass yield, baby corn provides a reliable source of green fodder throughout the year. The ample provision of vital nutrients in baby corn fodder contributes to enhanced digestion, improved rumen health, and increased milk production in dairy animals. As global consumers increasingly embrace healthy and diverse food choices, the demand for corn continues to expand, offering significant opportunities for both developed and developing nations (Boraiah *et al*., 2022; Yathish *et al*., 2022; Kumar *et al*., 2022; Kumar *et al*., 2021). To meet this demand there is a need to develop high-yielding and highly stable dual-purpose baby corn hybrids. Corn, being a cross-pollinated crop, offers immense potential for harnessing heterosis (Singh *et al*., 2021; Das *et al.,* 2021; Neelam *et al*., 2020). The presence of G × E interaction (GEI) necessitates the measurement of both performance and stability for any genotypes being evaluated in breeding programs (Devi *et al*., 2019; Rajora *et al*., 2017; Sah *et al*., 2016). This allows for a comprehensive assessment of the impact of GEI on phenotypic and genotypic values, avoiding potential biases in estimating heritability and predicting genetic advances. Two commonly used biplots for comprehending GEI analysis are the AMMI biplot (Gauch, 1992) and the genotype main effect plus genotype-environment interaction (GGE) biplot (Yan *et al*., 2000; Yan and Kang, 2003). The key distinction between the GGE biplot and the AMMI biplot lies in the fact that the GGE biplot eliminates the environment component and integrates the genotype with the GEI effect of a genotype-environment dataset (Yan *et al*., 2000). The multi-location testing aims to identify genotypes surpassing the commercial check-in target traits and to glean insights into stability and adaptability across varied environments. Consequently, this study examined the performance of dual-purpose baby corn hybrids with the specified objectives- (i) to estimate the GEI of baby corn hybrids, (ii) to identify high-yielding stable baby corn hybrids, and (iii) to classify the testing locations into mega-environments.

Materials and Methods

Plant materials and experimentation: The investigation involved the evaluation of 12 baby corn hybrids (Table 1) along with a commercial check, CMVL Baby corn 2, across four locations during the Rabi 2021-22. These four locations represented states falling under three distinct climatic zones, namely the northeastern plain zone (NEPZ; Varanasi and Hazaribagh), north-western plain zone (NWPZ; Ludhiana) and peninsular zone (PZ; Hyderabad) as defined by the All India Coordinated Research Project on Maize (Kumar *et al*., 2020a). The chosen multi-location testing in this experiment represented a variety of maize production ecosystems, which are distinguished by variations in latitude, altitude, and macro-climatic conditions. The locations were regarded as distinct environments where crops were cultivated using a complete randomized block design with three replications. In each replication, a crop geometry of 60 × 20 cm was used to sow each hybrid in four rows, each measuring four meters in length. Following germination, a population of 80 plants per plot was maintained in each replication. All the locations adhered to the standard recommended practices for crop management, as outlined by Kumar *et al.* (2020b).

Table 1. Details of genotypes used in the study

S. No.	Hybrid code	Pedigree/crosses
1.	T1	BIL9-1 × LM14
2.	T2	BIL9-1 × BML6
3.	T3	BIL9-1 × CML451
4.	T4	BIL9-1 × LM13
5	T5	BIL9-1 × IIMR 331
6	T6	BIL9-1 × CML286
7.	T7	BIL9-2 × CML451
8.	T8	BIL9-2 × LM14
9.	T9	BIL9-2 × BML6
10.	T10	BIL9-2 × LM 13
11.	T11	BIL9-2 × IIMR 331
12.	T12	BIL9-2 × CML 286

***Recording of observations*:** The 12 maize hybrids, along with the check, were evaluated for three traits viz., days to 50% silking (DS), baby corn yield (BCY; i.e., ears without husk) and green fodder yield (GFY; kg/plot)). Baby corn was harvested four days after silk emergence, and multiple pickings were taken for each hybrid. The represented data of days to 50% silking signifies the initial occurrence of 50% silk emergence for each hybrid. The data for BCY (kg/plot) were recorded as the combined weight of dehusked ears from multiple harvests. Following four rounds of picking, the green fodder was harvested, and its weight was measured in order to calculate the GFY, which accounted for the weight of husks from all pickings.

Data analysis: ANOVA was performed to analyze genotype (G), environment (E), and their interactions (GEI) using the agricolae package from the R statistical software in R Studio. Additive main effects and multiplicative interaction (AMMI) and GGE biplot analyses were conducted using the Agricolae and GGE Biplot GUI packages, respectively of the R statistical software in R Studio (R Studio, 2020). In the analysis of MLT data, no scaling was applied (‘scaling 0’ option) to generate a tester-centered (centering 2) GGE biplot as suggested by Yan and Tinker (2006). For genotype evaluation, genotype-focused singular value partitioning (SVP=1) was applied using the ‘Mean versus stability’ option of GGE biplot software, while environment-focused singular value partitioning (SVP=2) was employed (Yan, 2001) using Relation among testers’ option for environmental evaluation. The ‘Which-won-where’ option was utilized to identify the winning genotype within a given set of environments. To comprehend the intricate GEI, the integration of GGE biplot and AMMI analysis has emerged as a highly promising approach (Yan, 2001; Yan and Tinker, 2006). This combined methodology was followed to enable the graphical representation of the interaction pattern as well as to facilitate the identification of winning genotypes in specific environments and the delineation of mega-environments among different testing locations (Yan *et al*., 2007).

Results and Discussion

***Analysis of Variance*:** The multi-location testing selected for the present experiment reflected diverse maize production ecosystems characterized by differences in latitude, altitude, and macro-climatic conditions. The analysis of variance (ANOVA) indicated the significant influence of G, E, and GEI for all three traits studied in the experiment. The analysis revealed that the environmental factor accounted for a substantial proportion (86.72–95.59%) of the observed variation in the dataset, while the contributions of genotype (3.37–10.51%) and GEI (1.03–2.77%) were relatively minimal (Table 2). Notably, the contribution of G outweighed the contribution of GEI for all the traits, which suggested that the performance of genotypes was influenced to a lesser extent by environmental interaction. Similar findings with higher contribution of genotypes were reported earlier (Mohammadi *et al*., 2009). Among the traits, the environment had the greatest impact on DS, followed by BCY and GFY. When considering the mean values across different locations, the highest BCY was observed in Hazaribagh, while the highest GFY was recorded in Ludhiana. Conversely, Varanasi exhibited the lowest values for DS (indicating a preference for early genotypes) among the locations (Table 2). Similar findings were reported by Kumar *et al*. (2020b) and Chaudhary *et al*. (2019) for baby corn, where environmental factors contributed significantly (96.70-98.67%) to the observed variation. Likewise Rakshit *et al*. (2012) observed that location explained 59.3-89.9% of the total variation in sorghum.

Mean performance and stability of the genotypes across locations: The intricate interaction between genotypes and the environment could be effectively simplified and visualized using GGE biplot analysis, which represents the data graphically in different principal components (PCs) (Yan and Tinker, 2006). The first two PCs explained over 75% of the variation for all three traits, validating GGE biplots as accurate graphical representations of multi-location data. A cumulative variation of >60% (PC1 and PC2) provided a reliable approximation of the G × E variation (Yang *et al*., 2009; Yan *et al*., 2010). The graphical representation of PC1 and PC2 (Fig 1a-c) vividly depicted the complexity within the dataset. In the mean vs. stability graph, the line characterized by a single arrowhead represented the AEC abscissa. This line intersected the biplot origin and served as a marker for the average environment, progressing towards higher mean values. Additionally, the AEC ordinate, which was perpendicular to the AEC abscissa and passed through the biplot origin, played a crucial role. The length of the genotype's projection on the AEC ordinate reflected its stability, with longer projections indicating lesser stability. It was evident from the mean *vs.* stability graph that genotypes T11 and T9 outperform the check genotype T13, displaying the highest mean values for BCY and GFY. These high-performing genotypes also showed stability, with T9 exhibiting greater stability than T11 as indicated by its projection from the AEC abscissa. The delayed silk emergence in T9 and T11 compared to T13 suggested that these genotypes took more time in vegetative growth, leading to their higher yield. Thus T9 and T11 emerged as genotypes with both average stability and high yield for both traits BCY and GFY, possibly due to the influence of a shared set of genes. Following a similar approach, Kumar *et al.* (2020b), Chaudhary *et al.* (2019) and Magudeeswari *et*

Table 2. ANOVA and proportion of variation (G+E+GE) explained by genotype (G), environment (E) and GE interaction of three traits across the location with mean

Traits	MS value and % proportion of G, E & GE	Source of variation			Location wise mean (Unit: DS: days; BCY and GFY: kg/plot)			
		G	E	GE	Hazaribagh	Varanasi	Ludhiana	Hyderabad
DS	MS	14.08***	398.39**	4.28***	67.88	68.80	74.30	75.73
	Proportion of G+E+GE (%)	3.37	95.59	1.03				
BCY	MS	1.28**	11.84***	0.254*	2.10	1.59	1.83	1.94
	Proportion of G+E+GE (%)	9.57	88.53	1.90				
GFY	MS	27.12***	223.73**	7.15***	19.22	19.66	25.56	22.47
	Proportion of G+E+GE (%)	10.51	86.72	2.77				

*** *P<0.001, ** P<0.01, *P<0.05*

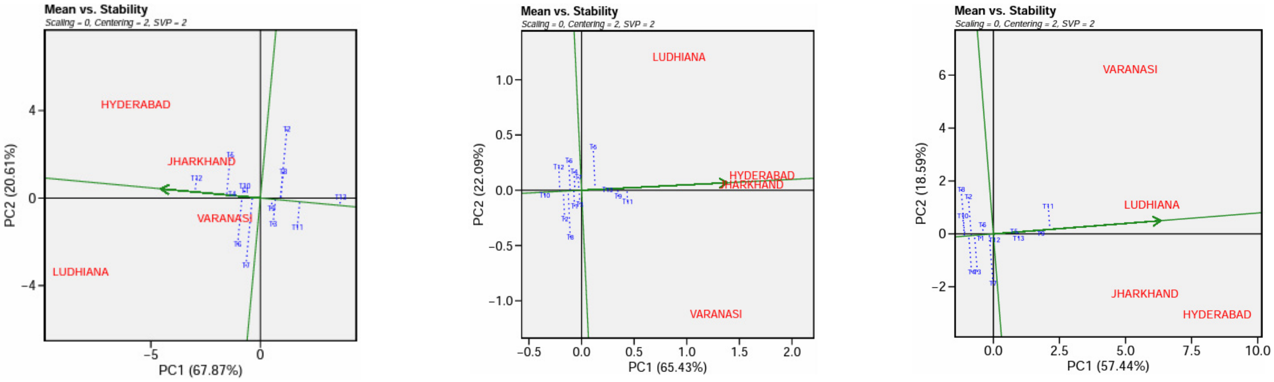

Fig 1a. Mean *vs.* stability (Days to 50% silking)

Fig 1b. Mean *vs.* stability (Baby corn yield)

Fig 1c. Mean *vs.* stability (Green fodder yield)

Fig 1. Mean performance and stability of genotypes for studied parameters (DS, BCY and GFY)

al. (2023) observed high-performing and stable genotypes in baby corn.

***Genotypic and environmental evaluation*:** One major advantage of the graphical presentation of GEI is the facile identification of genotypes that are closer to the ideal genotype (Yan and Tinker, 2006). The same applies to identifying the ideal environment. The ideal genotype, characterized by high yield and greater stability, is represented by the longest vector length of the highest-yielding genotype with zero GEI, located at the center of the concentric circles (Fig 2a-b). Based on this study, it could be concluded that genotypes T9, T11, and T13 closely approached the ideal genotype for both BCY and GFY traits. Furthermore, these three genotypes outperformed the check in terms of mean performance and stability (Fig 2a-b).

The graphical representation of biplots also facilitates the interpretation of the interaction between testing environments through the angle between their vectors. The line connecting the marker of an environment to the origin of the biplot represents the vector of that environment, and the cosine of the angle between two vectors indicates their correlation (Yan and Tinker, 2006). Analysis of the BCY and GFY traits revealed acute vector angles representing all four locations: Varanasi, Hazaribagh, Hyderabad and Ludhiana (Fig 3a-b). The angle between Hyderabad and Hazaribagh was much smaller than their angles with Ludhiana and Varanasi. Acute vector angles show a closer relationship between environments (Yan and Tinker, 2006). Therefore, out of the four locations, the environments of Hyderabad and Hazaribagh exhibited a strong correlation, while the correlation between Ludhiana and Varanasi was comparatively weaker, as indicated by the nearly right angle between them (Fig 3a-b). This revealed that genotypes that performed well in one environment might exhibit poor performance in another, while closer relationships among different locations indicated the absence of crossover GE, showing consistent genotype rankings across locations (Rao *et al.*, 2011). This phenomenon could be attributed to the fact that some genotypes responded to environmental variation while others displayed stability because of the combined properties of their gene combinations. Consequently, the four testing locations could be grouped into three mega-environments: Group I, comprising Hyderabad and Hazaribagh; Group II represented by Ludhiana, and group III, encompassing Varanasi.

***Which won where and mega environment identification*:** A 'which-won-where' graph was constructed by connecting the most distant genotypes, thus forming a polygon in the biplot. Subsequently, perpendicular lines were drawn from the origin of the biplot to each side of the polygon, effectively dividing the biplot into distinct sectors with one genotype positioned at each vertex of the polygon. These lines were referred to as equality lines (Yan, 2001). The genotypes at the vertices of the polygon represented the best performers in the environments falling within their respective sectors (Yan, 2002; Yan and Tinker, 2006). The 'which-won-where' feature of the GGE biplot was a crucial aspect that graphically explained crossover GE, differentiation of mega-environments, and specific adaptation (Yan *et al.*, 2000; Yan and Tinker, 2006; Putto *et al.*, 2008; Rao *et al.*, 2011). Based on this analysis, the partitioning of testing locations into three mega-environments (Group I as Hyderabad and Hazaribagh, Group II as Ludhiana, and Group III represented Varanasi) was confirmed.

For the BCY trait, the 'which-won-where' plot identified T11 as the winning genotype in both group I and group III mega-environments, while T5 emerged as the winning genotype for the group II mega-environment. For the GFY trait, T9 and T11 were the winning genotypes in group I and group III mega-environments (Fig 4a-b). This

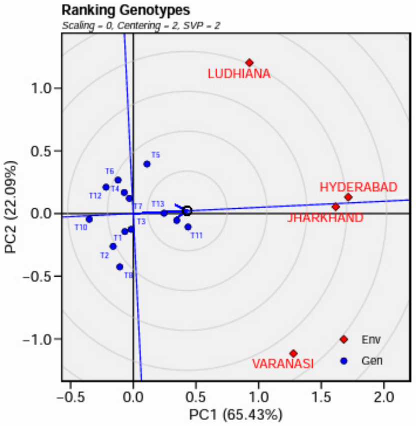

Fig 2a. Ideal genotype (Baby corn yield)

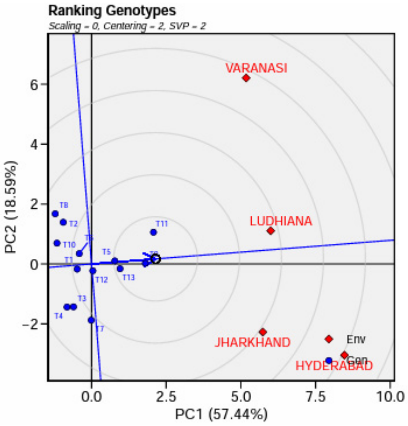

Fig 2b. Ideal genotype (Green fodder yield)

Fig 2. Genotypic evaluation for ranking of genotypes and identification of ideal genotypes

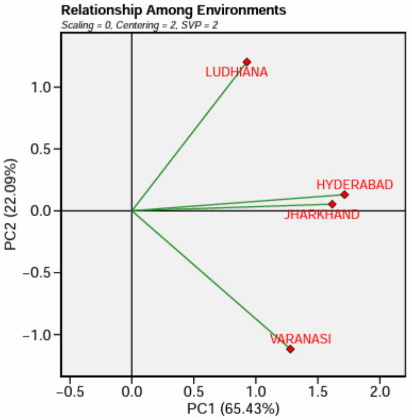

Fig 3a. Environmental relation (Baby corn yield)

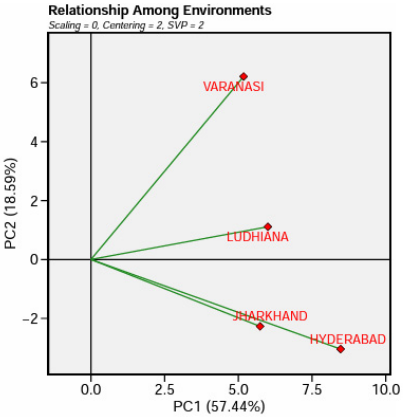

Fig 3b. Environmental relation (Green fodder yield)

Fig 3. Relationship among environments based on environmental evaluation

suggested that although testing was conducted at multiple locations, similar results could be obtained from one or two representatives of each mega-environment. However, it was essential to verify this mega-environment pattern through multi-year and multi-environment trials, as recorded in studies involving wheat (Yan *et al*., 2000) and peanut (Putto *et al*., 2008).

AMMI analysis: The analysis of variance (ANOVA) conducted in additive main effects and multiplicative interaction (AMMI) analysis revealed significant differences (p <0.01) for environments (E), genotypes (G), and the GEI for all the traits (Table 2). The significant effect of the GEI indicated genotypes performed differently across various environments. The AMMI analysis conducted for the three traits across three environments highlighted the predominant contribution of the environment to the total variation, surpassing the contributions of genotype and GEI. The significant proportion of the sum of squares attributed to environmental factors implies notable variations in means of specific environments, which predominantly explains the observed variability in all traits. The outcome of the AMMI analysis was confirmed by the GGE biplot in this study. The AMMI1 (PC1 *vs.* additive effects from varieties and environment) and AMMI2 (PC2 *vs.* PC1) biplot graphs provide insights into the main effects of traits and principal components (Fig 5a-b; 6a-b).

In the AMMI1 biplot, the abscissa and ordinate axes represent the trait main effect and the first principal component (PC1) term, respectively. Genotypes with PC1 scores close to zero indicated general adaptation across environments, while larger PC1 scores indicated specific adaptation to environments with the same PC1 score and sign (Murphy *et al*., 2009). Our analysis revealed that the group II environment (Ludhiana) exhibited the lowest BCY, while the lowest GFY values were observed in the group I environment (Hazaribagh and Hyderabad). The dispersion of environmental effects on the biplot exceeded the scores of varietal effects, indicating greater variability resulting from environmental factors compared to genotypic effects (Fig 5a-b; 6a-b). Following Duarte and Vencovsky (1999), stability is assessed on the y-axis (PC1) in the AMMI1 analysis, while the AMMI2 analysis

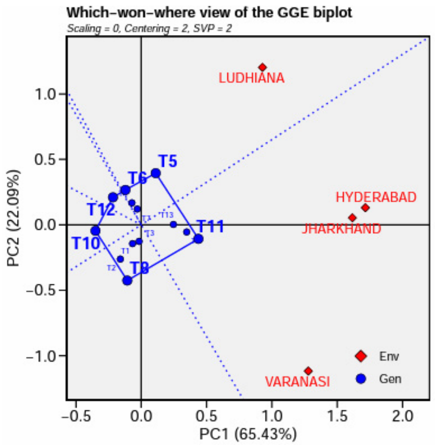

Fig 4a. Which won where (Baby corn yield)

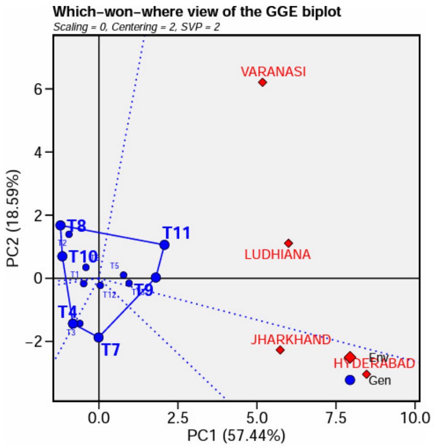

Fig 4b. Which won where (Green fodder yield)

Fig 4. Which won where and mega environment identification for baby corn and green fodder yields

identifies stable environments and genotypes positioned near the origin. Based on AMMI1 analysis, genotype T13 displayed the highest stability for BCY. However, high-yielding genotypes T11 and T9 were also situated closer to the axis, indicating their stability for BCY. For GFY, genotypes T5, T13, T11, and T9 exhibited both high yields and stability across locations, as evidenced by their proximity to the axis and smaller contribution to the GEI. In the AMMI2 analysis, the biplot employs the first and second principal component terms (PC1 and PC2) as the abscissa and ordinate, respectively. The biplot is divided into four sectors by horizontal and vertical lines intersecting at the origin (0, 0). Locations closer to the biplot origin indicate less interaction and are considered favorable for selecting genotypes with average adaptation (Murphy *et al.*, 2009). The angle between genotype and environment vectors determines the nature of GEI: acute angles indicate positive interaction, right angles indicate negligible interaction and obtuse angles indicate negative interaction. Additionally, the distance of

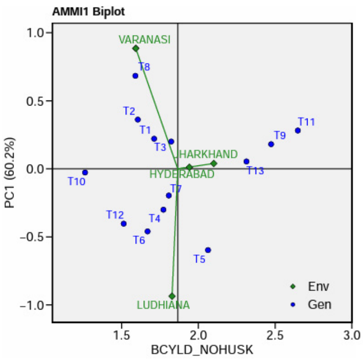

Fig 5a. AMMI I biplot (Baby corn yield)

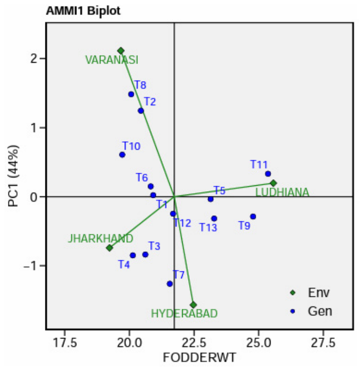

Fig 5b. AMMI I biplot (Green fodder yield)

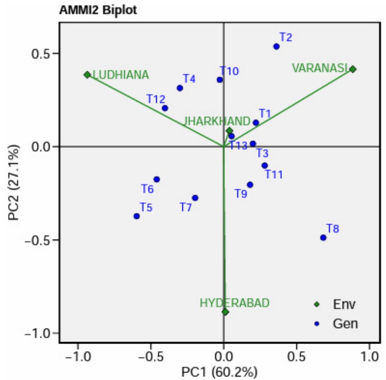

Fig 6a. AMMI II biplot (Baby corn yield)

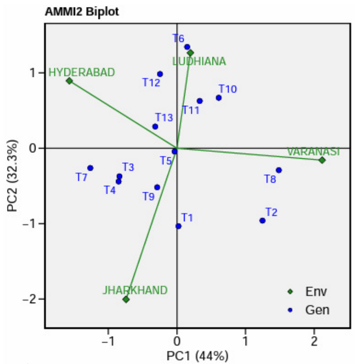

Fig 6b. AMMI II biplot (Green fodder yield)

Fig 5-6. AMMI I and AMMI II biplot analysis for baby corn and green fodder yields genotype and environment vectors from the biplot origin reflects the magnitude of GEI exhibited by genotypes or environments. For both traits, the four locations fell into distinct sectors. Through AMMI2 analysis, genotypes T5, T9, T13, and T11 were identified as the most stable. The AMMI2 biplot provides more precise information as it incorporates PC1 and PC2 data, offering a more comprehensive representation compared to the AMMI1 biplot, which solely considers PC1. According to the AMMI2 analysis, Varanasi contributed significantly to the phenotypic stability of genotypes for both BCY and GFY traits (Fig 6a-b).

Conclusion

According to the GGE biplot and AMMI analysis, it was inferred that the environmental assessment could categorize the locations into three distinct mega-environments. Genotypes T9 and T11 exhibited superior performance and stability across multiple locations for both BCY and GFY traits. These genotypes possess the capability to not only augment farmers' earnings through baby corn cultivation but also aid in addressing the scarcity of green fodder in the nation. Given the significant improvement in yields compared to the control variety, these genotypes can be subjected to further testing in AICRP trials to explore their potential for release. Furthermore, the parental inbred lines of these two hybrids can be employed in breeding programs, utilizing different mating designs with other elite inbred lines that demonstrate high yields in both baby corn and green fodder.

References

Anonymous. 2015. *IGFRI Vision 2050*. Indian Grassland and Fodder Research Institute, Jhansi, India.

Boraiah, K. M., P. S. Basavaraj, M. H. Hanamant, G. Mukri, K. R. Yathish, N. R. Prakash and S. Kumar. 2022. Maize: impacts and management of abiotic stresses. In: H. Pathak (ed). *Abiotic Stresses in Agriculture: Impacts and Management*. ICAR-National Institute of Abiotic Stress Management, Pune, India. pp. 116-150.

Chaudhary, M., B. Kumar, P. Kumar, S. K. Guleria, N. K. Singh, R. Khulbe and S. Rakshit. 2019. GGE biplot analysis of genotype × environment interaction and identification of mega-environment for baby corn hybrids evaluation in India. *Indian Journal of Genetics and Plant Breeding* 79: 658-669.

Das, A. K., M. Choudhary, P. Kumar, C. G. Karjagi, K. R. Yathish, R. Kumar and S. Rakshit. 2021. Heterosis in genomic era: advances in the molecular understanding and techniques for rapid exploitation. *Critical Reviews in Plant Sciences* 40: 218-242.

Devi, R., V. K. Sood, H. K. Chaudhary, A. Kumari and A. Sharma. 2019. Identification of promising and stable genotypes of oat (*Avena sativa* L.) for green fodder yield under varied climatic conditions of north-western Himalayas. *Range Management and Agroforestry* 40: 67-76.

Duarte, J.B. and R. Vencovsky. 1999. Genotype × environment interaction: an introduction to AMMI analysis = Interaçãogenótipos × ambientes: umaintrodução à análise AMMI. *Sociedade Brasileira de Genética, RibeirãoPreto*, SP, Brazil (in Portuguese).

Gauch, H.G. 1992. AMMI analysis of yield trials. In: M.S. Kang and H.G. Gauch (eds). *Genotype-by-Environment Interaction.* CRC Press. Boca Raton. pp. 1-40.

Ghosh, P. K., D. R. Palsaniya and R. Srinivasan. 2016. Forage research in India: issues and strategies. *Agricultural Research Journal* 53: 1-12.

Hossain, F., V. Muthusamy, J. S. Bhat, R. U. Zunjare, S. Kumar, N. R. Prakash and B. K. Mehta. 2022. Maize breeding. In: D. K. Yadav, H. K. Dikshit, G. P. Mishra and S. Tripathi (eds). *Fundamentals of Field Crop Breeding*. Springer Nature, Singapore. pp. 221-258.

Kumar, B., M. Choudhary, K. Kumar, P. Kumar, S. Kumar, P. K. Bagaria and S. Rakshit. 2022. Maydis leaf blight of maize: update on status, sustainable management and genetic architecture of its resistance. *Physiological and Molecular Plant Pathology* 121: 101889. https://doi.org/10.1016/j.pmpp.2022.101889.

Kumar, B., S. Rakshit, N. Suni., R. Kumar, S. B. Singh, G. K. Chikkappa, J. C. Sekhar, S. L. Jat, S. K. Agarwal, A. K. Singh, L. P. Soujanya and S. B. Suby. 2020a. Standard operating practices for testing of maize entries in All India Coordinate Research Project Trials. ICAR-Indian Institute of Maize Research, Ludhiana. pp. 1-94.

Kumar, P., M. Choudhary, B. S. Jat, M. C. Dagla, V. Singh, A. K. Das and S. H. Wani. 2021. Isolation of genes/quantitative trait loci for drought stress tolerance in maize. In: M. A. Hossain, M. Alam, S. Seneweera, S. Rakshit and R. Henry (eds). *Molecular Breeding in Wheat, Maize and Sorghum: Strategies for Improving Abiotic Stress Tolerance and Yield*. CABI, Wallingford, UK. pp. 267-281.

Kumar, P., S. Kumar, M. Choudhary, G. K. Chikappa, B. Kumar, N. K. Singh and S. K. Sinha. 2020b. GGE biplot based stability analysis of experimental hybrids for baby corn purpose and green fodder. *Range Management and Agroforestry* 41: 60-66.

Magudeeswari, P., E. V. D. Sastry and T. R. Devi. 2023. Variability and stability analyses for yield and related traits of baby corn (*Zea mays* L.) genotypes grown under NE region of India. *Electronic Journal of Plant Breeding* 14: 471-479.

Mohammadi, R., M. Aghaee, R. Haghparast, S. S. Pourdad, M. Rostaii, Y. Ansari, A. Abdolahi and A. Amri. 2009. Association among non-parametric measures of phenotypic stability in four annual crops. *Middle Eastern and Russian Journal of Plant Science and Biotechnology* (Special Issue I): 20-24.

Murphy, S. E., E. A. Lee., L. Woodrow., P. Seguin., J. Kumar., I. Rajcan., and G. R. Ablett. 2009. Genotype x environment interaction and stability for isoflavone content in soybean. *Crop Science* 49:1313–1321. doi:10.2135/cropsci2008.09.0533.

Neelam, S., R. K. Tyagi, S. Pandey, S. R. Jacob, C. S. Javaji, M. K. Debnath and S. Kumar. 2020. Comprehending the diversity in the regenerated set of maize (*Zea mays* L.) landraces conserved in the Indian national genebank. *Indian Journal of Plant Genetic Resources* 33: 329-333.

Putto, W., A. Patanothai, S. Jogloy and Hoogenboom. 2008. Determination of mega-environments for peanut breeding using the CSM-CROPGRO-Peanut model. *Crop Science* 48: 973-982.

R Studio Team. 2020. R Studio: Integrated Development for R. R Studio, PBC, Boston, MA URL *http://www.rstudio.com/*.

Rajora, M. P., C. S. Shantharaja, P. K. Roy, M. Patidar and R. K. Bhatt. 2017. Stability analysis for forage yield in *Cenchrus ciliaris* under hot arid climate. *Range Management and Agroforestry* 38: 191-198.

Rakshit, S., K. N. Ganapathy, S. S. Gomashe, A. Rathore, R. B. Ghorade, M. V. K. Nagesh, K. Ganesmurthy, S. K. Jain, M. Y. Kamtar, J. S. Sachan, S. S. Ambekar, B. R. Ranwa, D. G. Kanawade, M. Balusamy, D. Kadam, A. Sarkar, V. A. Tonapi and J. V. Patil. 2012. GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. *Euphytica* 185: 465-479.

Rao, P. S., P. S. Reddy, A. Ratore, B. V. S. Reddy and S. Panwar. 2011. Application GGE biplot and AMMI model to evaluate sweet sorghum (*Sorghum bicolor*) hybrids for genotype x environment interaction and seasonal adaptation. *Indian Journal of Agricultural Sciences* 81: 438-444.

Sah, R. P., S. Ahmed, D. R. Malaviya and P. Saxena. 2016. Identification of consistence performing dual purpose maize (*Zea mays* L.) genotypes under semi-arid condition. *Range Management and Agroforestry* 37: 162-166.

Singh, S. B., P. Kumar, R. K. Kasana, M. Choudhary, S. Kumar, R. Kumar and S. Rakshit. 2021. Unveiling combining ability and heterotic grouping of newly developed winter maize (*Zea mays*) inbreds. *Indian Journal of Agricultural Sciences* 91: 1586-1591.

Yan, W. 2001. GGE biplot–a windows application for graphical analysis of multi-environment trial data and other types of two-way data. *Agronomy Journal* 93: 1111-1118.

Yan, W. 2002. Singular value partitioning for biplot analysis of multi-environment trial data. *Agronomy Journal* 4: 990-996.

Yan, W. and M. S. Kang. 2003. *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists*. CRC Press. Boca Raton.

Yan, W. and N. A. Tinker. 2006. Biplot analysis of multi-environment trial data: principles and applications. *Canadian Journal of Plant Science* 86: 623-645.

Yan, W., J. Fregeau-Reid, D. Pageau, R. Martin, J. Mitchell-Fetch, M. Etieenne, J. Rowsell, P. Scott, M. Price, B. de Hann, A. Cummiskey, J. Lajeunesse, J. Durand and E. Sparry. 2010. Identifying essential test location for oat breeding in eastern Canada. *Crop Science* 50: 504-515.

Yan, W., L. A. Hunt, Q. Sheng and Z. Szlavnics. 2000. Cultivar evaluation and mega-environment investigation based on GGE biplot. *Crop Science* 40: 597-605.

Yan, W., M. S. Kang, B. L. Ma, S. Woods and P. L. Cornelius. 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. *Crop Science* 47: 643-653.

Yang, R.C., J. Crossa, P.L. Cornelius and J. Burgueno. 2009. Biplot analysis of genotype × environment interaction: proceed with caution. *Crop Science* 49: 1564-1576.

Yathish, K. R., C. G. Karjagi, S. S. Gangoliya, A. Kumar, J. Preeti, H. K. Yadav and R. N. Gadag. 2022. Introgression of the low phytic acid locus (lpa2) into elite maize (*Zea mays L.*) inbreds through marker-assisted backcross breeding (MABB). *Euphytica* 218: 127. https://doi.org/10.1007/s10681-022-03076-y.